Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1.–26. (Canceled)

27. (Currently Amended) A method ~~Method~~ for detecting ~~a~~ microorganism contamination in a culture of eukaryotic cells to be used for gene expression profiling, the method comprising:

(a) providing a microarray which has attached on its surface:

(i) ~~(a.1)~~ at least one nucleic acid probe representing a gene of the ~~a~~ eukaryotic cell, and

(ii) ~~(a.2)~~ at least one nucleic acid probe representing a gene of a microorganism,

(b) preparing nucleic acid targets from said culture by means of a primer mixture suitable for amplifying said at least one gene of a eukaryotic cell and said at least one gene of a microorganism,

(c) contacting the microarray of step (a) with the nucleic acid targets of step (b) to permit selective hybridization between the nucleic acid targets and their complementary nucleic acid probes on the microarray, and

(d) correlating the selective hybridization between the nucleic targets and the at least one nucleic acid probe representing a gene of the microorganism with the presence of ~~detecting said hybridization thereby detecting~~ ~~a~~ microorganism contamination and, optionally, detecting the expression of genes specific for the eukaryotic cell.

28. (Previously Presented) The method according to claim 27, the method comprising an additional step:

(e) comparing the gene expression of contaminated eukaryotic cells with the gene expression of non-contaminated eukaryotic cells.

29. (Previously Presented) The method according to claim 27, wherein the microorganism belongs to the class of mollicutes.

30. (Previously Presented) The method according to claim 27, wherein the microorganism is selected from the group consisting of Mycoplasma, Ureaplasma, Acholeplasma and Spiroplasma.

31. (Previously Presented) The method according to claim 27, wherein the microorganism is Mycoplasma.

32. (Previously Presented) The method according to claim 27, wherein the nucleic acid probe representing a gene of the microorganism and the primer specific for the microorganism comprises a nucleic acid sequence of the 16S or 23S rRNA gene, preferably the 16S or 23S rRNA of mycoplasma.

33. (Previously Presented) The method according to claim 27, wherein the nucleic acid probe representing a gene of the microorganism and the primer specific for the microorganism comprises a nucleic acid sequence of the 16S or 23S rRNA gene comprising a sequence as defined by SEQ ID NOs: 1, 3, 4 or 5.

34. (Currently Amended) The method according to claim 27, wherein the ~~preparing~~ preparation of a nucleic acid target sample in step (b) of claim 27~~1~~ includes an in vitro transcription reaction, preferably wherein the in vitro transcription is mediated by the use of primers comprising the sequence of the T7 promoter, the T3 promoter or the SP6 promoter, wherein the T7 promoter is preferably the T7 promoter as defined by SEQ ID NO:2.

35. (Previously Presented) The method according to claim 27, wherein the eukaryotic cells are mammalian cells, preferably human cells.

36. (Withdrawn - Currently Amended) A microarray which has attached on its surface:

(a) ~~(a.1)~~ at least one nucleic acid probe representing a gene of a eukaryotic cell, and

(b) ~~(a.2)~~ at least one nucleic acid probe representing a gene of a microorganism.

37. (Withdrawn - Currently Amended) The microarray according to claim 36, wherein the nucleic acid probe in (b) ~~(a.2)~~ comprises a sequence of the 16S rRNA gene, preferably of mycoplasma, preferably as defined by SEQ ID NO:1.

38. (Withdrawn) A diagnostic kit for detecting the presence of a microorganism in a cell culture, the kit comprising a microarray as defined in claim 36, a suitable primer mixture, suitable enzymes, optionally labelled rNTPs, and a positive template control.

39. (Previously Presented) The method according to claim 27, wherein the method is for analyzing the effect of a microorganism contamination on the gene expression of eukaryotic cells, and wherein step

(d) comprises detecting said hybridization thereby detecting the expression of genes specific a eukaryotic cells and detecting said microorganism contamination,

and wherein the method comprises step

(e) comparing the gene expression of contaminated eukaryotic cells with the gene expression of non-contaminated eukaryotic cells, wherein an altered expression of one or more genes is indicative of an effect of the microorganism on the expression of said genes.

40. (Previously Presented) The method according to claim 27, wherein the method is for testing the suitability of a culture of eukaryotic cells for gene expression profiling by detecting the absence or presence of a microorganism, and wherein step

(d) comprises detecting said hybridization thereby detecting the absence or presence of a microorganism, wherein the absence indicates the suitability of said cell culture for gene expression profiling,

and wherein said method comprises optionally an additional step:

(e) using the microarray of step c) for gene expression profiling provided the absence of a microorganism has been detected.

41. (Previously Presented) The method according to claim 27, wherein the method is for testing the suitability of a culture of eukaryotic cells for gene expression profiling by detecting the absence or presence of a microorganism, and wherein the culture of eukaryotic cells, an extract or fraction thereof, is used for gene expression profiling, and wherein step

(d) comprises detecting said hybridization thereby detecting the absence or presence of a microorganism, wherein the absence indicates the suitability of said cell culture for gene expression profiling,

and wherein said method comprises optionally an additional step:

(e) using the microarray of step c) for gene expression profiling provided the absence of a microorganism has been detected,

42. (Currently Amended) A method (i) for detecting ~~a~~ microorganism contamination in a culture of eukaryotic cells to be used for gene expression profiling, or (ii) for analyzing by gene expression profiling the effect of ~~a~~ microorganism contamination on the gene expression of eukaryotic cells, or (iii) for gene expression profiling by detecting the absence or presence of a microorganism,[[.]] wherein the method comprises ~~comprising~~ the ~~step~~ steps of:

(a) preparing nucleic acid targets by use of a primer comprising a ~~the~~ nucleic acid sequence complementary to a ~~the~~ target region of the ~~a~~ microorganism, and

(b) wherein the gene expression profiling is done by using a microarray which has attached on its surface:

(i) at least one nucleic acid probe representing a gene of a eukaryotic cell, and

(ii) at least one nucleic acid probe representing a gene of a microorganism.

43. (Previously Presented) The method according to claim 42, wherein the target region of a microorganism is 16S rRNA, preferably the 16S rRNA of Mycoplasma.

44. (Cancelled)

45. (Currently Amended) The method according to claim 42, wherein the detecting of a microorganism contamination in a culture of eukaryotic cells to be used for gene expression profiling is done by using a microarray which has attached on its surface:

(a) ~~(a.1)~~ at least one nucleic acid probe representing a gene of a eukaryotic cell, and

(b) ~~(a.2)~~ at least one nucleic acid probe representing a gene of a microorganism.